

ENTERED

See p.6



PCT09

#13

RAW SEQUENCE LISTING

DATE: 07/11/2002

PATENT APPLICATION: US/09/647,140A

TIME: 13:24:25

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt

Output Set: N:\CRF3\07112002\I647140A.raw

```

3 <110> APPLICANT: Fox Chase Cancer Center
4     Kruh, Gary D.
5     Lee, Kun
6     Belinsky, Martin G.
7     Bain, Lisa J.
9 <120> TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
10    Nucleic Acids and Methods of Use Thereof
12 <130> FILE REFERENCE: FCCC 98-02
14 <140> CURRENT APPLICATION NUMBER: 09/647,140A
15 <141> CURRENT FILING DATE: 2001-05-21
17 <150> PRIOR APPLICATION NUMBER: PCT/US99/06644
18 <151> PRIOR FILING DATE: 1999-03-26
20 <150> PRIOR APPLICATION NUMBER: 60/079,759
21 <151> PRIOR FILING DATE: 1998-03-27
23 <150> PRIOR APPLICATION NUMBER: 60/095,153
24 <151> PRIOR FILING DATE: 1998-08-03
26 <160> NUMBER OF SEQ ID NOS: 18
28 <170> SOFTWARE: FastSEQ for Windows Version 3.0
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 4231
33 <212> TYPE: DNA
34 <213> ORGANISM: Homo sapiens
36 <400> SEQUENCE: 1
37  ggacaggcgt ggcgcccgga gccccagcat ccctgcttga ggtccaggag cggagcccg 60
38  ggccaccgcc gctgatcag cgcgaccccg gccgcgccc gccccgccg gcaagatgct 120
39  gcccggtgtac caggagggtga agcccaaccc gctgcaggac gcgaacatct gctcacgcgt 180
40  gttcttctggt tggctcaatc ccttgtttaa aattggccat aaacggagat tagaggaaga 240
41  tgatatgtat tcagtgtgc cagaagaccg ctacagcac cttggagagg agttgcaagg 300
42  gttctgggat aaagaagttt taagagctga gaatgacgca cagaagcctt ctttaacaag 360
43  agcaatcata aagtgttact ggaaatctta tttagttttg ggaattttta cgttaattga 420
44  ggaaagtgcc aaagtaatcc agcccatatt tttggaaaa attattaatt attttgaaaa 480
45  ttatgatccc atggattctg tggttttgaa cacagcgtac gcctatgcca cgggtgctgac 540
46  tttttgcacg ctcatcttgg ctatactgca tcaattatat ttttatcacg ttcagtgtgc 600
47  tgggatgagg ttacgagtag ccattgtgcca tatgatttat cggaaggcac ttcgtcttag 660
48  taacatggcc atggggaaga caaccacagg ccagatagtc aatctgctgt ccaatgatgt 720
49  gaacaagttt gatcagggtga cagtgttctt acacttcctg tgggcaggac cactgcaggc 780
50  gatcgagctg actgccctac tctggatgga gataggaata tcgtgccttg ctgggatggc 840
51  agttctaatc attctcctgc ccttgcaaag ctgttttggg aagttgttct catcactgag 900
52  gagtaaaact gcaactttca cggatgccag gatcaggacc atgaatgaag ttataactgg 960
53  tataaggata ataaaaatgt acgcctggga aaagtcattt tcaaacttta ttaccaattt 1020
54  gagaaagaag gagatttcca agattctgag aagttcctgc ctacggggga tgaatttggc 1080
55  ttcgtttttc agtgcaagca aaatcatcgt gtttgtgacc ttcaccacct acgtgtcct 1140
56  cggcagtggt atcacagcca gccgcgtgtt cgtggcagtg acgctgtatg gggctgtgcg 1200

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57	gctgacgggtt	accctcttct	tcccctcagc	cattgagagg	gtgtcagagg	caatcgtcag	1260
58	catocgaaga	atccagacct	ttttgctact	tgatgagata	tcacagcgca	accgtcagct	1320
59	gcogtcagat	ggtaaaaaga	tggtgcatgt	gcaggatttt	actgcttttt	gggataaggc	1380
60	atcagagacc	ccaactctac	aaggcctttc	ctttactgtc	agacctggcg	aattgttagc	1440
61	tgtggtcggc	cccggtggag	caggggaagtc	atcactgtta	agtgccgtgc	tcggggaatt	1500
62	ggccccaagt	cacgggctgg	tcagcgtgca	tggaagaatt	gcctatgtgt	ctcagcagcc	1560
63	ctgggtgttc	tcgggaactc	tgaggagtaa	tattttattt	gggaagaaat	atgaaaagga	1620
64	acgatatgaa	aaagtcataa	aggcttgtgc	tctgaaaaag	gatttacagc	tggttgagga	1680
65	tggtgatctg	actgtgatag	gagatcgggg	aaccacgctg	agtggagggc	agaaagcacg	1740
66	ggtaaacctt	gcaagagcag	tgtatcaaga	tgctgacatc	tatctcctgg	acgatcctct	1800
67	cagtgcagta	gatgcggaag	ttagcagaca	cttgttcgaa	ctgtgtattt	gtcaaatttt	1860
68	gcatgagaag	atcacaattt	tagtgactca	tcagttgcag	tacctcaaag	ctgcaagtca	1920
69	gattctgata	ttgaaagatg	gtaaaatggg	gcagaagggg	acttacactg	agttcctaaa	1980
70	atctggtata	gattttggct	ccctttttaa	gaaggataat	gaggaaagtg	aacaacctcc	2040
71	agttccagga	actcccacac	taaggaatcg	taccttctca	gagtcttcgg	tttgggtctca	2100
72	acaatcttct	agacctcctt	tgaaagatgg	tgctctggag	agccaagata	cagagaatgt	2160
73	cccagttaca	ctatcagagg	agaaccgttc	tgaaggaaaa	gttggttttc	aggcctataa	2220
74	gaattacttc	agagctgggt	ctcactggat	tgtcttcatt	ttccttattc	tcctaaacac	2280
75	tgacgtcag	gttgccatg	tgcttcaaga	ttggtggcct	tcatactggg	caaacaaaca	2340
76	aagtatgcta	aatgtcactg	taaatggagg	aggaaatgta	accgagaagc	tagatcttaa	2400
77	ctggtactta	ggaattttatt	caggtttaac	tgtagctacc	gttctttttg	gcatagcaag	2460
78	atctctattg	gtattctacg	tccttggtta	ctcttcacaa	actttgcaca	acaaaatggt	2520
79	tgagtcaatt	ctgaaagctc	cgggtattatt	ctttgataga	aatccaatag	gaagaatttt	2580
80	aaatcgtttc	tccaaagaca	ttggacactt	ggatgatttg	ctgccgctga	cgtttttaga	2640
81	tttcatccag	acattgctac	aagtgggttg	tgtggtctct	gtggctgtgg	ccgtgattcc	2700
82	ttggatcgca	atacccttgg	ttccccttgg	aatcattttc	atttttcttc	ggcgatattt	2760
83	tttgaaacg	tcaagagatg	tgaagcgctt	ggaatctaca	actcggagtc	cagtgttttc	2820
84	ccacttgtea	tcttctctcc	aggggctctg	gaccatccgg	gcatacaaa	cagaagagag	2880
85	gtgtcaggaa	ctgtttgatg	cacaccagga	tttacattca	gaggcttggg	tcttgttttt	2940
86	gacaacgtcc	cgctggttcg	ccgtccgtct	ggatgccatc	tgtgccatgt	ttgtcatcat	3000
87	cgttgccctt	gggtccctga	ttctggcaaa	aactctggat	gccgggcagg	ttggtttggc	3060
88	actgtcctat	gccctcacgc	tcattgggat	gtttcagtgg	tgtgttcgac	aaagtgcgtga	3120
89	agttgagaat	atgatgatct	cagtagaaa	ggtcattgaa	tacacagacc	ttgaaaaaga	3180
90	agcaccttgg	gaatatcaga	aacgcccacc	accagcctgg	ccccatgaag	gagtataaat	3240
91	ctttgacaat	gtgaacttca	tgtacagtcc	aggtgggcct	ctggtactga	agcatctgac	3300
92	agcactcatt	aaatcacaag	aaaagggttg	cattgtggga	agaaccggag	ctggaaaaag	3360
93	ttccctcatc	tcagcccttt	ttagattgtc	agaaccggaa	ggtaaaattt	ggattgataa	3420
94	gatcttgaca	actgaaattg	gacttcacga	tttaagggaag	aaaatgtcaa	tcatacctca	3480
95	ggaacctgtt	ttgttctactg	gaacaatgag	gaaaaacctg	gatcccttta	aggagcacac	3540
96	ggatgaggaa	ctgtggaatg	ccttacaaga	ggtacaactt	aaagaaacca	ttgaagatct	3600
97	tcctggtaaa	atggatactg	aattagcaga	atcaggatcc	aatttttagtg	ttggacaaag	3660
98	acaactgggtg	tgctttgcc	gggcaattct	caggaaaaat	cagatattga	ttattgatga	3720
99	agcgacggca	aatgtggatc	caagaactga	tgagttaata	caaaaaaaaa	tccgggagaa	3780
100	atttgccac	tgaccctgct	taaccattgc	acacagattg	aacaccatta	ttgacagcga	3840
101	caagataatg	gttttagatt	caggaagact	gaaagaatat	gatgagccgt	atgttttgct	3900
102	gcaaaataaa	gagagcctat	tttacaagat	ggtgcaacaa	ctgggcaagg	cagaagccgc	3960
103	tgccctcact	gaaacagcaa	aacagggtata	cttcaaaaga	aattatccac	atattggtca	4020
104	cactgaccac	atggttacaa	acacttccaa	tggacagccc	tcgaccttaa	ctattttcga	4080
105	gacagcactg	tgaatccaac	caaatgtca	agtccgttcc	gaaggcattt	tccactagtt	4140

RAW SEQUENCE LISTING

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Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt

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106  ttggaactat gtaaaccaca ttgtactttt ttttactttg gcaacaaata tttatacata      4200
107  caagatgcta gttcatttga atatttctcc c                                     4231
110  <210> SEQ ID NO: 2
111  <211> LENGTH: 1325
112  <212> TYPE: PRT
113  <213> ORGANISM: Homo sapiens
115  <400> SEQUENCE: 2
116  Met Leu Pro Val Tyr Gln Glu Val Lys Pro Asn Pro Leu Gln Asp Ala
117      1          5          10          15
118  Asn Ile Cys Ser Arg Val Phe Phe Trp Trp Leu Asn Pro Leu Phe Lys
119      20          25          30
120  Ile Gly His Lys Arg Arg Leu Glu Glu Asp Asp Met Tyr Ser Val Leu
121      35          40          45
122  Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp
123      50          55          60
124  Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu
125      65          70          75          80
126  Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser Tyr Leu Val Leu Gly
127      85          90          95
128  Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val Ile Gln Pro Ile Phe
129      100         105         110
131  Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr Asp Pro Met Asp Ser
132      115         120         125
133  Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr Val Leu Thr Phe Cys
134      130         135         140
135  Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr Phe Tyr His Val Gln
136      145         150         155         160
137  Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys His Met Ile Tyr Arg
138      165         170         175
139  Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly Lys Thr Thr Thr Gly
140      180         185         190
141  Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn Lys Phe Asp Gln Val
142      195         200         205
143  Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro Leu Gln Ala Ile Ala
144      210         215         220
145  Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile Ser Cys Leu Ala Gly
146      225         230         235         240
147  Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln Ser Cys Phe Gly Lys
148      245         250         255
149  Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr Phe Thr Asp Ala Arg
150      260         265         270
151  Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile Arg Ile Ile Lys Met
152      275         280         285
153  Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile Thr Asn Leu Arg Lys
154      290         295         300
155  Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys Leu Arg Gly Met Asn
156      305         310         315         320
157  Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile Val Phe Val Thr Phe
158      325         330         335

```

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```

159 Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr Ala Ser Arg Val Phe
160          340          345          350
161 Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu Thr Val Thr Leu Phe
162          355          360          365
163 Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg
164          370          375          380
165 Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg
166          385          390          395          400
167 Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr
168          405          410          415
169 Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser
170          420          425          430
171 Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly
172          435          440          445
173 Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro
174          450          455          460
175 Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln
176          465          470          475          480
177 Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly
178          485          490          495
179 Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala
180          500          505          510
181 Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile
182          515          520          525
183 Gly Asp Arg Gly Thr Pro Leu Ser Gly Gly Gln Lys Ala Arg Val Asn
184          530          535          540
185 Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp
186          545          550          555          560
187 Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu
188          565          570          575
189 Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His
190          580          585          590
191 Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp
192          595          600          605
193 Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly
194          610          615          620
196 Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln
197          625          630          635          640
198 Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu
199          645          650          655
200 Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly
201          660          665          670
202 Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu
203          675          680          685
204 Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr
205          690          695          700
206 Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu
207          705          710          715          720
208 Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser

```

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209						725										735
210	Tyr	Trp	Ala	Asn	Lys	Gln	Ser	Met	Leu	Asn	Val	Thr	Val	Asn	Gly	Gly
211				740					745					750		
212	Gly	Asn	Val	Thr	Glu	Lys	Leu	Asp	Leu	Asn	Trp	Tyr	Leu	Gly	Ile	Tyr
213			755					760					765			
214	Ser	Gly	Leu	Thr	Val	Ala	Thr	Val	Leu	Phe	Gly	Ile	Ala	Arg	Ser	Leu
215		770					775						780			
216	Leu	Val	Phe	Tyr	Val	Leu	Val	Asn	Ser	Ser	Gln	Thr	Leu	His	Asn	Lys
217	785					790					795					800
218	Met	Phe	Glu	Ser	Ile	Leu	Lys	Ala	Pro	Val	Leu	Phe	Phe	Asp	Arg	Asn
219					805					810						815
220	Pro	Ile	Gly	Arg	Ile	Leu	Asn	Arg	Phe	Ser	Lys	Asp	Ile	Gly	His	Leu
221				820					825					830		
222	Asp	Asp	Leu	Leu	Pro	Leu	Thr	Phe	Leu	Asp	Phe	Ile	Gln	Thr	Leu	Leu
223			835					840						845		
224	Gln	Val	Val	Gly	Val	Val	Ser	Val	Ala	Val	Ala	Val	Ile	Pro	Trp	Ile
225		850					855						860			
226	Ala	Ile	Pro	Leu	Val	Pro	Leu	Gly	Ile	Ile	Phe	Ile	Phe	Leu	Arg	Arg
227	865					870					875					880
228	Tyr	Phe	Leu	Glu	Thr	Ser	Arg	Asp	Val	Lys	Arg	Leu	Glu	Ser	Thr	Thr
229					885					890						895
230	Arg	Ser	Pro	Val	Phe	Ser	His	Leu	Ser	Ser	Ser	Leu	Gln	Gly	Leu	Trp
231				900					905						910	
232	Thr	Ile	Arg	Ala	Tyr	Lys	Ala	Glu	Glu	Arg	Cys	Gln	Glu	Leu	Phe	Asp
233			915					920						925		
234	Ala	His	Gln	Asp	Leu	His	Ser	Glu	Ala	Trp	Phe	Leu	Phe	Leu	Thr	Thr
235		930					935						940			
236	Ser	Arg	Trp	Phe	Ala	Val	Arg	Leu	Asp	Ala	Ile	Cys	Ala	Met	Phe	Val
237	945					950					955					960
238	Ile	Ile	Val	Ala	Phe	Gly	Ser	Leu	Ile	Leu	Ala	Lys	Thr	Leu	Asp	Ala
239					965					970						975
240	Gly	Gln	Val	Gly	Leu	Ala	Leu	Ser	Tyr	Ala	Leu	Thr	Leu	Met	Gly	Met
241				980					985					990		
242	Phe	Gln	Trp	Cys	Val	Arg	Gln	Ser	Ala	Glu	Val	Glu	Asn	Met	Met	Ile
243			995					1000						1005		
244	Ser	Val	Glu	Arg	Val	Ile	Glu	Tyr	Thr	Asp	Leu	Glu	Lys	Glu	Ala	Pro
245		1010					1015						1020			
246	Trp	Glu	Tyr	Gln	Lys	Arg	Pro	Pro	Pro	Ala	Trp	Pro	His	Glu	Gly	Val
247	1025					1030						1035				1040
248	Ile	Ile	Phe	Asp	Asn	Val	Asn	Phe	Met	Tyr	Ser	Pro	Gly	Gly	Pro	Leu
249																

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/11/2002
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 18
Seq#:16; N Pos. 4,7,10,13,16,19
Seq#:17; N Pos. 23,29
Seq#:18; N Pos. 9,18

VERIFICATION SUMMARY

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Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt

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L:1178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:1287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:1320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:1352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0